

Publication

A virtual look at Epstein-Barr virus infection: simulation mechanism

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Epstein-Barr virus (EBV) is an important human pathogen that establishes a life-long persistent infection and for which no precise animal model exists. In this paper, we describe in detail an agent-based model and computer simulation of EBV infection. Agents representing EBV and sets of B and T lymphocytes move and interact on a three-dimensional grid approximating Waldeyer's ring, together with abstract compartments for lymph and blood. The simulation allows us to explore the development and resolution of virtual infections in a manner not possible in actual human experiments. Specifically, we identify parameters capable of inducing clearance, persistent infection, or death.

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